
MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
on: Fri May 14 08:07:02 1999; MasPar time 158.91 Seconds
Regular output not generated. 861.291 Million cell updates/sec
Title: >US-08-911-423-3
Description: (1-1006) from US08911423.seq
Perfect Score: 1006
N.A. Sequence: 1 ATGGCACACACAGGGCGCAT.....ACACGTCCTGACTGGGAAA 1006
Comp: TACCGTGTGTGTCGCCGCTA.....TGTTGACGAGTACCCCTTT
Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 188442 seqs, 68026449 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40
Statistics: Mean 8.82; Variance 5.749; scale 1.547
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40
Statistics: Mean 8.82; Variance 5.749; scale 1.547
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
C 1	114	11.3	3327	30	T69936	Coprinus cinereus lac 1.47e-52
2	96	9.5	2606	14	Q83277	P. falciparum E3la ge 2.05e-41
3	96	9.5	2606	32	T72895	Plasmodium E3la gene. 2.05e-41
4	85	8.4	1581	22	T32233	Cuphea C14:0-ACP thio 1.08e-34
5	71	7.1	533	38	V02890	Human HMG1-C aberrant 2.80e-26
6	65	6.5	774	38	V02893	Human HMG1-C aberrant 9.86e-23
7	59	5.9	757	38	V02898	Human HMG1-C aberrant 3.12e-19
8	43	4.3	91	9	Q51746	Oligonucleotide probe 3.27e-10
9	42	4.2	91	9	Q51746	Oligonucleotide probe 1.14e-09
C 10	42	4.2	204	1	N81164	Base substituted E.co 1.14e-09
11	41	4.1	178	32	T76405	Human endothelin-1 an 3.97e-09
12	39	3.9	204	1	N81164	Base substituted E.co 4.89e-08
C 13	39	3.9	206	23	T27694	pgEM32f target fragme 4.69e-08

C 14	39	3.9	206	37	T70340	DNA substrate for 5'	4.69e-08
C 15	39	3.9	228	13	Q80775	5' Nuclease substrate	4.69e-08
C 16	39	3.9	349	23	T27571	Human TSH beta-chain	4.69e-08
C 17	39	3.9	969	40	T99561	Polynucleotide encodi	4.69e-08
C 18	39	3.9	1287	3	N40087	Sequence from phage M	4.69e-08
C 19	39	3.9	1287	3	N50326	Phage M13tg910 used i	4.69e-08
C 20	39	3.9	1380	2	Q11381	T. hyo gene 6:lacZ fu	4.69e-08
C 21	39	3.9	1619	12	Q71364	Expression cassette c	4.69e-08
C 22	39	3.9	1754	12	Q71365	Expression cassette c	4.69e-08
C 23	39	3.9	2027	25	T42137	I2C-4 gene encoding F	4.69e-08
C 24	39	3.9	3198	38	T92869	Candida carhol gene.	4.69e-08
C 25	39	3.9	3212	40	V03313	Archaeoglobus lithotr	4.69e-08
C 26	39	3.9	3681	2	Q13578	Plasmid PKSEL5.	4.69e-08
C 27	39	3.9	3699	39	V14340	Plasmid pBSGFP expres	4.69e-08
C 28	39	3.9	4118	35	T59189	Construct pGEM-hTR(Ka	4.69e-08
C 29	39	3.9	4118	35	T69188	Construct pGEM-hTR co	4.69e-08
C 30	39	3.9	4164	16	T04575	Plasmid pAT-1 sequenc	4.69e-08
C 31	39	3.9	4274	9	Q54144	Sequence of plasmid p	4.69e-08
C 32	39	3.9	4283	37	T86610	Epidermal growth fact	4.69e-08
C 33	39	3.9	4283	35	T86449	DNA encoding hGH, EGF	4.69e-08
C 34	39	3.9	4539	14	Q87347	Plasmid pINVI.	4.69e-08
C 35	39	3.9	4771	38	V02186	Human type C lectin e	4.69e-08
C 36	39	3.9	4792	15	Q84696	Plasmid GS contg. N.	4.69e-08
C 37	39	3.9	4933	16	T04569	Plasmid pAT-2 sequenc	4.69e-08
C 38	39	3.9	5042	15	Q84694	Plasmid glucoamylase	4.69e-08
C 39	39	3.9	6824	6	Q39050	K.lactis/S. cerevisae	4.69e-08
C 40	39	3.9	7287	39	V02042	Plasmid pWRG3169 enco	4.69e-08
C 41	39	3.9	9837	38	T96851	Intron 21 of human pR	4.69e-08
C 42	39	3.9	10306	12	Q73734	Retro virus vector p5	4.69e-08
C 43	39	3.9	10930	20	Q81226	Plasmid pMI6-1.	4.69e-08
C 44	39	3.9	10950	20	O81225	Plasmid pMI6.	4.69e-08
C 45	39	3.9	10970	12	Q73735	Retro virus vector p5	4.69e-08

ALIGNMENTS

RESULT 1
ID T69936 standard; DNA; 3327 BP.
AC T69936;
DT 21-JUL-1997 (first entry)
DE Coprinus cinereus lacase lcc1 genomic DNA.
KW Benzenediol:oxygen oxidoreductase; laccase; lignin; Kraft pulp; dye;
KW fungus; polymerase chain reaction; papermaking; ss.
OS Coprinus cinereus (strain IFO 8371).
FH Key Location/Qualifiers
FT exon 1..851
FT /*tag= a
FT /*number= 1
FT /*codon_start= 726
FT intron 852..906
FT /*tag= b
FT /*number= 1
FT /*cons_splice= (5'site:YES,3'site:YES)
FT /*note= "The printed version of the sequence has the
FT following splice junction sequences (with
FT exon nucleotides shown in capitals and intron
FT nucleotides shown in lower case):
FT 5' site:GC/gt and 3' site:ag/TG"
FT exon 907..1023
FT /*tag= c
FT /*number= 2
FT intron 1024..1100
FT /*tag= d
FT /*number= 2
FT /*cons_splice= (5'site:YES,3'site:YES)
FT /*tag= e
FT /*number= 3
FT intron 1249..1316
FT /*tag= f
FT /*number= 3
FT /*cons_splice= (5'site:NO,3'site:NO)
FT /*note= "The printed version of the sequence has the


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RESULT 3
ID T72895 standard; cDNA; 2606 BP.
AC T72895;
DT 07-OCT-1997 (first entry)
DE Plasmodium E31a gene.
KW DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
KW Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
KW DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
KW Plasmodium; ss.
OS Plasmodium falciparum.
FH Key Location/Qualifiers
FT cds 106..2460
FT /tag= a
FT /note= *encodes residues 1-785 of W22480*
PN WO9640766-A2.
PD 19-DEC-1996.
PF 07-JUN-1996; U09508.
PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;
PI Wellem's TE;
PI WPI: 97-052231/05.
DR P-PSDB; W22480.
DR New malaria vaccines - contains cysteine-rich DBL family protein
PT binding domains homologous domains of the Duffy and sialic acid
PT binding proteins
PS Disclosure; Page 43; 96pp; English.
CC This sequence represents the E31a gene of Plasmodium. E31a belongs to
CC the Duffy binding like (DBL) family of genes which have homology to the
CC Duffy antigen binding protein (DABP) and sialic acid binding protein
CC (SABP) conserved regions (see T72889 and T72888 respectively). The var
CC family of genes modulate cytoadherence and antigenic variation of
CC Plasmodium infected erythrocytes. SABP and the Duffy antigen binding
CC protein (DABP) are soluble proteins that appear in the culture
CC supernatant after infected erythrocytes release merozoites. DABP and SABP
CC mediate the binding of merozoites and schizonts to the erythrocyte
CC surface. These proteins are necessary for erythrocyte invasion by the
CC parasite. This sequence can be used in the compositions of the invention.
CC The compositions are for the treatment and prevention of malaria, and
CC comprise either a nucleotide sequence or encoded polypeptide of the
CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of
CC genes having homology with conserved regions of DABP and SABP. The
CC compositions are used for the treatment and prevention of malaria. They
CC are also used in the preparation of vaccines for inducing a protective
CC immune response in a mammal to Plasmodium merozoites (especially
CC Plasmodium falciparum or Plasmodium vivax).
CC Sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
CC Query Match 9.5%; Score 96; DB 32; Length 2606;
CC Best Local Similarity 99.0%; Pred. No. 2.05e-41;
CC Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dd 2455 caagctacgctcgctgacgctacgctacgctcttcttagtgcacctaattcaaa 2514
|||||
Qy 909 CAAGCTTAGGTACGGTGCATCGGACGATAGCTTCTTATAGTGTACCTAAATTCAA 968
|||||

Dd 2515 ttcactggcgcgtcgttttacaacgctgactgggaaa 2552
|||||
Qy 969 TTCACCTGGCGGCTGTTTACAAACGCTCCTGACTGGGAAA 1006
|||||

RESULT 4
ID T32233 standard; cDNA; 1581 BP.
AC T32233;
DT 26-OCT-1996 (first entry)
DE Cuphea C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2).
KW Myristate; myristic acid; fatty acid; acyl-ACP thioesterase;
KW seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
KW surfactant; ss.
OS Cuphea palustris.
FH Key Location/Qualifiers
FT cds 119..1354

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FT WO9623892-A2.
PN 08-AUG-1996.
PD 01-FEB-1996; U01585.
PF 02-FEB-1995; US-383756.
PR 05-JUN-1995; US-460898.
PA (CALJ ) CALGENE INC.
PI Dehesh K, Hawkins D, Voelker TA;
PI WPI: 96-371439/37.
DR P-PSDB; W02081.
DR Recombinant prodn. of myristate in plant cells - using DNA with
PT preferential activity on C14 fatty acids from Cuphea palustris,
PT nutmeg and camphor, useful in detergent and food industries
PS Example 1; Fig 1A-1E; 77pp; English.
CC A cDNA clone (T32233), designated MCT34 (pCpFatB2), codes for Cuphea
CC palustris C14:0-ACP thioesterase (W02081), an enzyme that acts
CC primarily on C14:0-ACP substrates, forming C14:0 (myristate). It
CC was isolated from a developing seed cDNA library by screening with
CC sequences encoding medium-chain acyl-ACP thioesterases from Cuphea
CC hookeriana. Constructs for expression of clone MCT34 in plant seeds
CC under the control of napin or oleosin regulatory regions were prepd.
CC These allow high-level prodn. of myristate (useful in surfactants
CC and foods) in plant cells, e.g. Brassica.
CC Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;
CC Query Match 8.4%; Score 85; DB 22; Length 1581;
CC Best Local Similarity 98.9%; Pred. No. 1.08e-34;
CC Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dd 1495 ggcggcgctctagagatcccaagcttaagtcgctgacgctacgctctctt 1554
|||||
Qy 889 GGGGGCGGCTCTAAAGATCCCAAGCTTACGTACGCGTGACGTCATAGCTCTCT 948
|||||

Dd 1555 atagtgcacctaaattcaattcaactg 1581
|||||
Qy 949 ATAGTGTCACTAAATTCATTCACCTG 975
|||||

RESULT 5
ID V02890 standard; cDNA; 533 BP.
AC V02890;
DT 08-MAY-1998 (first entry)
DE Human HMGI-C aberrant form 11.
KW High mobility group protein; HMGI-C; MAG; human; treatment; modulator;
KW multiple tumour aberration growth gene; vascular development;
KW angiogenesis; vascularisation; endometriosis; contraception
KW tissue regeneration; ss.
OS Homo sapiens.
PN DE19548122-A1.
PD 26-JUN-1997.
PF 21-DEC-1995; 048122.
PR 21-DEC-1995; DE-048122.
PI (BULL/) BULLERDIEK J.
PI Bullerdiek J;
PI WPI: 97-333837/31.
DR DNA sequences representing aberrant forms of human high mobility
PT group protein genes - useful for treatment of endometriosis and
PT tumours, or for modulating vascularisation, etc
PS Claim 1; Fig 11; 58pp; German.
CC V02880-V02898 are cDNA sequences that encode aberrant forms of the human
CC high mobility group protein (HMG) gene, HMGI-C, which is located on
CC chromosome 12. These sequences encode the DNA binding part of the
CC translation product but not the protein binding domain. These proteins,
CC antibodies derived from these proteins or expression modulators of the
CC HMGI-C protein can be used in kits to modulate vascular development. Such
CC kits can reduce, block or stimulate angiogenesis or vascularisation and
CC can improve vascular provision in myocardium damaged by infarction. Such
CC proteins can also be used to treat endometriosis and tumours, for
CC contraception (local or oral) and for tissue regeneration, especially in
CC degenerating or damaged tissue. The regeneration method can be applied to
CC tissues which are currently impossible or difficult to regenerate and the
CC use of biological material with attendant risks of viral transmission and
CC anaphylactic shock, is avoided.

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tissue regeneration; ss.

KW Homo sapiens.
OS DE19548122-A1.
PN 26-JUN-1997. 048122.
PD 21-DEC-1995; 048122.
PF 21-DEC-1995; DE=048122.
PR (BULL/) BULLERDIEK J.
PA Bullerdiek J;
PI WPI: 97-333837/31.
DR DNA sequences representing aberrant forms of human high mobility
PT group protein genes - useful for treatment of endometriosis and
PT tumours, or for modulating vascularisation, etc

PS Claim 1; Fig 19; 58pp; German.
CC V02880-V02898 are cDNA sequences that encode aberrant forms of the human
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CC kits can reduce, block or stimulate angiogenesis or vascularisation and
CC can improve vascular provision in myocardium damaged by infarction. Such
CC proteins can also be used to treat endometriosis and tumours, for
CC contraception (local or oral) and for tissue regeneration, especially in
CC degenerating or damaged tissue. The regeneration method can be applied to
CC tissues which are currently impossible or difficult to regenerate and the
CC use of biological material with attendant risks of viral transmission and
CC anaphylactic shock, is avoided.
SQ Sequence 797 BP; 267 A; 178 C; 181 G; 167 T;

Query Match 5.9%; Score 59; DB 38; Length 797;
Best Local Similarity 96.8%; Pred. No. 3.12e-19;
Matches 61; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dbb 735 ggcggcgcttaagatccaaacttacgtacggtcattcatgcacgatcgttcgtct 794
QY 889 ggccgccgcctctaaggatccaagttagcttaccggttgatcgacgtcatgcacctct 948
Db 795 ata 797
QY 949 ATA 951

RESULT 8
ID Q51746 standard; cdna; 91 bp.
AC Q51746;
DT 31-MAY-1994 (first entry)
DE Oligonucleotide probe MK14-A
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW ss.
OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI: 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial spp. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 4.3%; Score 43; DB 9; Length 91;
Best Local Similarity 12.7%; Pred. No. 3.27e-10;
Matches 8; Conservative 45; Mismatches 10; Indels 0; Gaps 0;

Dbb 1 qgcctccgccgssbvsvvvvhhvbhbhvhsvvvvvhvhhvvbhvvhhvvhhvvsv 60

CC DNA-polymerases to cleave a specific sequence structure
 CC was tested using the duplex sequence given in Q80775 and
 CC the pilot oligonucleotides given in Q80758-60.
 SQ Sequence 228 BP; 59 A; 56 C; 53 G; 60 T;
 Query Match 3.9%; Score 39; DB 13; Length 228;
 Best Local Similarity 97.6%; Pred. No. 4.69e-08;
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 10 ttccccagtcacgacgttgtataaacgacgacgcccagtggaattg 50
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Cp 1006 TTCCCGAGTCAGGACGTTGTAAACGACGCGCCAGTGAATTG 966

Search completed: Fri May 14 08:09:48 1999
 Job time : 166 secs.

W O R L D

(TM)

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Comp: TACCGTGTGTCGCCCGCTA.....TGTTCGAGGACTGACCCCTT

Scoring table:
Gap 6
TABLE default

Nmatch STD : Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb157
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_un 15:em_vi
Database: genbank110
16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov
22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1
27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy
33:gb_un 34:gb_vi

Statistics: Mean 10.691; Variance 5.553; scale 1.925

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	228	22.7	1020 29	Mus musculus glucocort	2.35e-151
2	116	11.5	4109 33	Cloning vector pSPORT1	1.95e-63
3	106	10.5	4310 33	Cloning vector pSPORT2	7.72e-56
4	85	8.4	1581 22	Sequence 1 from patent	3.80e-40
5	82	8.2	5772 24	Saccharomyces cerevisi	6.09e-38
6	70	7.0	2699 34	HIV-1 strain W02 from	3.04e-29
7	68	6.8	98 27	Human hepg2 3' region	8.14e-28
8	63	6.3	538 22	Sequence 1 from patent	2.80e-24
9	59	5.9	398 31	human STS SHGC-2867 cl	1.74e-21
10	58	5.8	433 31	LSCV119 Caprine BAC Ca	8.55e-21
11	57	5.7	3160 32	Cloning vector pSVSPORT	4.19e-20
12	56	5.6	1297 24	Cucumis sativus mRNA f	2.04e-19
13	55	5.5	414 31	human STS SHGC-6182 cl	9.85e-19

C	14	55	2746 32	CVPGEM42	Cloning vector pGEM-42	9.85e-19
15	54	5.4	390 31	G16894	human STS SHGC-3196 cl	4.74e-18
16	412	4.8	412 31	G17976	human STS SHGC-3315 cl	5.04e-14
17	48	4.8	7218 22	I66494	Sequence 14 from patent	5.04e-14
18	45	4.5	1359 29	MUSHAPTGB	Mus saxicola haptoglob	4.68e-12
19	44	4.4	965 22	AR024229	Sequence 22 from patent	2.08e-11
20	41	4.1	215 22	I28278	Sequence 5 from patent	1.72e-09
21	41	4.1	346 31	G41210	LSCV116 Caprine BAC Ca	1.72e-09
22	41	4.1	7218 22	I66494	Sequence 14 from patent	1.72e-09
23	40	4.0	2860 32	AF017063	Cloning vector pMECA,	7.32e-09
24	40	4.0	4498 16	ECY10544	Cloning vector pKIL194	7.32e-09
25	39	3.9	1287 22	A04663	Phage M13tg910.	3.08e-08
26	39	3.9	2886 19	CPU69698	Cryptosporidium parvum	3.08e-08
27	39	3.9	2958 32	ARBLKSP	pBluescript KS(+) vect	3.08e-08
28	39	3.9	2958 32	ARBLKSP	pBluescript SK(+) vect	3.08e-08
29	39	3.9	3199 32	CVGEM32FM	Cloning vector pGEM-32	3.08e-08
30	39	3.9	3223 32	CVGEM112P	Cloning vector pGEM-11	3.08e-08
31	39	3.9	3570 32	CVU39779	Cloning vector pTRIPLE	3.08e-08
32	39	3.9	4091 19	PL18SRNA	P.lividus gene for 18S	3.08e-08
33	39	3.9	4190 32	XXU13848	pEXcell cloning vector	3.08e-08
34	39	3.9	4539 22	I18794	Sequence 1 from patent	3.08e-08
35	39	3.9	4670 24	ATHAVPEA	Arabidopsis thaliana g	3.08e-08
36	39	3.9	4788 32	CVU73899	Cloning vector pJB3, c	3.08e-08
37	39	3.9	5314 22	A20700	pMTV1 DNA sequence.	3.08e-08
38	39	3.9	5967 32	EVU84006	Expression vector pBSI	3.08e-08
39	39	3.9	6170 32	U02457	Cloning vector pYEBra3	3.08e-08
40	39	3.9	7372 32	SVNPHSCSKV	Phagescript SK cloning	3.08e-08
41	39	3.9	7507 32	CVU51113	Cloning vector pBeloBA	3.08e-08
42	39	3.9	21013 27	D78345	Human DNA for Ig gamma	3.08e-08
43	39	3.9	94882 18	AC02317	*** SQUENCING IN PROG	3.08e-08
44	39	3.9	167846 18	CEY56C5	Caenorhabditis elegans	3.08e-08
45	39	3.9	256175 18	HS437G10	Human DNA sequence ***	3.08e-08

ALIGNMENTS

RESULT	1	MMU82534	1020 bp	MRNA	ROD	18-OCT-1997
LOCUS		Mus musculus glucocorticoid induced TNFR family related protein precursor, mRNA, complete cds.				
DEFINITION		U82534				
ACCESSION		92228583				
NID						
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 1020)				
AUTHORS		Nocentini,G., Giunchi,L., Ronchetti,S., Krausz,L.T., Bartoli,A., Moraca,R., Miglioni,G. and Ricciardi,C.				
TITLE		A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis				
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6216-6221 (1997)				
MEDLINE		97322352				
REFERENCE		2 (bases 1 to 1020)				
AUTHORS		Nocentini,G., Giunchi,L., Ronchetti,S., Krausz,L.T., Bartoli,A., Moraca,R., Miglioni,G. and Ricciardi,C.				
TITLE		Direct Submission				
JOURNAL		Submitted (18-DEC-1996) Carlo Ricciardi, Clinical Medicine, Pathology and Pharmacology, Perugia University, V. del Giochetto, Perugia, PG 06100, Italy				
FEATURES		Location/Qualifiers				
source		1..1020				
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		/strain="C3H/HeN"				
		/db_xref="taxon:10090"				
		/cell_type="thymocytes"				
		46..732				
CDS		/note="type I transmembrane protein; belongs to the tumor necrosis factor receptor/nerve growth factor receptor family"				
		/codon_start=1				
		/product="glucocorticoid induced TNFR family related				

protein precursor"					
/db_xref="PID:g2228584"					
/translation="MGAWAMLVGVSMCLVDLQSPVVEPCCGPGKVQGSGNNTRFC					
CSLYAPKEDCKERICVTPEYKHCPQCGPKTKHYPCQPQGORVESQGDIVFGRCVA					
CANGTFSAGDRGCHRLWNCISGFGLTFMFGKNTHNAVCIPEPLPTPEOXYGHILTVFLV					
MAACIFELTTVLQLGIHWLRQHMCMPRETQPPAEVLASADACSFQFPFEERGEQTE					
EKCHLGGRWP"					
46..102					
sig_peptide					
mat_peptide					
103..729					
/notes="type I transmembrane protein"					
/product="glucocorticoid induced TNFR family related					
protein"					
misc_feature					
103..504					
/note="-encodes extracellular domain"					
misc_feature					
127..228					
/note="encodes TNFR cystein repeat 1"					
misc_feature					
229..348					
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misc_feature					
349..471					
/note="encodes TNFR cystein repeat 3"					
misc_feature					
505..573					
/note="encodes transmembrane domain"					
misc_feature					
574..729					
/note="encodes intracellular domain"					
BASE COUNT					
231 a 269 c 292 g 228 t					
ORIGIN					
Query Match 22.7%; Score 228; DB 29; Length 1020;					
Best Local Similarity 72.1%; Pred. No. 2.35e-151;					
Matches 372; Conservative 0; Mismatches 144; Indels 0; Gaps 0;					
Db	176	GCTGCAGCCTGTATGCTCCAGGCAAGGAGGACTGTCAAAAGAAGAGTGATATGTGCA	235		
Qy	167	GCTGCTCCGGATTACC CGGCGAGGAGTGCTGTTCCGAGTGGAGTGCATGTGTCTC	226		
Db	236	CACCTGAGTACCACTGTGGAGACCCCTCAGTGCAAGATCTGCAAGCATACCCCTGCCAAC	295		
Qy	227	AGCCTGAATTCACCTGCGGAGACCCCTTGCTGCACGAGCTGCCGCGCACCCCTTGTCCCC	286		
Db	296	CAGGCCAAGGGTGGAGTCTCAAGGGATATGTTGGCTTCCGGTGTGTCCTGCTG	355		
Qy	287	CAGGCCAAGGGGTACAGTCCCAGGGGAATTCAGTTTTGGCTTCAGTGTATCAGCTGTG	346		
Db	356	CCATGGGCACCTTCTCCGCAAGTCTGACGCTCACTGCAGACTTTGGACCAACTGTTCTC	415		
Qy	347	CCTCGGGACCTTCTCGGGGGCCACGAAGCCACTGCAAACTTGGACAGACTGCACCC	406		
Db	416	AGTTTGATTTCTCACCATGTTCCCTGGGACACAGACCCACAATGCTGTGTGCATCCGG	475		
Qy	407	AGTTGGGGTTCTCACATGTGTGTTCCCTGGGAACAGACCCACAACGCTGTGTGCTCCAG	466		
Db	476	AGCCACTTCCCACTGAGCAATACGCCATTTGACTGTGTCATCTTCTGTCTATGCTGCTCAT	535		
Qy	467	GGTCCCGCGCGCAGACCGCTTGGTGGCTGACCGTCTCTCTCTGCGCGTGGCCGCT	526		
Db	536	GCATTTTCTTCTTAACACAGTCCAGCTCGGCTTGACATATGCGATGAGGAGGCAAC	595		
Qy	527	CGCTCCCTCTCTGACCTCGGCCACGCTTGACATGCAATCTGCGAGCTGAGGAGTCACT	586		
Db	596	ACATGTGCTCTCGAGAGACCCACCATTCGCGGAGGTGTCAGTTGTCAGCTCAGGATGCTT	655		
Qy	587	GCATGTGCGCCCGAGAGACCCAGCTGCTGTGTGAGGTGCGCCCGCTCGNCCAGACGCCA	646		
Db	656	GCAGCTTCCAGTTCCCTTGAGGAGGAACCGGGGAGC	691		
Qy	647	GAAGCTGCCAGTTTCCCGGAAGAGAGCGGGGCGAGC	682		

RESULT	2	PSORT1	4109 bp	DNA	UNA	23-AUG-1994
LOCUS						
DEFINITION		Cloning vector psport1, complete cds.				
ACCESSION		U12390				
NTD		q531828				

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KEYWORDS          Cloning vector pSport1.
SOURCE            Cloning vector pSport1
ORGANISM          artificial sequence; cloning vectors.
REFERENCE         1 (sites)
AUTHORS           D'Alessio,J.M., Gruber,C.E., Cain,C. and Noon,M.C.
TITLE            Construction of Directional cDNA Libraries Using the Superscript
JOURNAL           Plasmid System
REFERENCE         2 (bases 1 to 4109)
AUTHORS           Horton,M. E.
TITLE            Direct Submission
JOURNAL           Submitted (18-JUL-1994) Horton M. E., Life Technologies, Inc.,
                  Technical Services, 8400 Helgeman Court, Gaithersburg, MD
                  20884-9980, USA
FEATURES          Location/Qualifiers
SOURCE            1..4109
                  /organism="Cloning vector pSport1"
                  /db_xref="taxon:36386"
                  complement(<1..341)
                  /codon_start=1
                  /transl_table=11
                  /evidence=experimental
                  /product="beta-galactosidase alpha peptide"
                  /db_xref="PID:g531829"
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                  YACMRHSSIVSPKFNLSLAVLQRDWPNGVTQLNRLAAHPFASFARNSEARTDR
                  PSQQLRSLNGEX"
SOURCE            1..4109
                  /organism="unidentified"
                  /plasmid="pSport1"
                  /db_xref="taxon:32644"
                  /lab_host="Escherichia coli"
                  complement(125..147)
                  /standard_name="M13/pUC 23 base forward sequencing primer"
                  complement(150..161)
                  /standard_name="M13/pUC forward sequencing primer"
                  /evidence=experimental
                  164..180
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                  /evidence=experimental
                  191..285
                  /function="multiple cloning site"
                  /evidence=experimental
                  complement(298..318)
                  /note="T7 promoter"
                  /evidence=experimental
                  complement(464..1546)
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                  /evidence=experimental
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                  LNTIPNVAQLAGKQSLIGVATSSIALHAPQIVAAIKSRADQICASVSVSVMSVES
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                  FSHEDGTGLVHEHLVAGHQIALLAGPLSVSARLWAGHKYLTNRQIQPIAERG
                  DWSAMSGFTQMTLMNEGIVPTAMLVANDQALMGALRAITEGLRGLVADGISVVGDDQT
                  EDSSCYTPPTTQKDFPRLIGQTSVDRLLQLSQGVAKGNQLLPVSVISVKRKTTLAPNT
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                  complement(1896..1902)
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                  /evidence=experimental
                  complement(2661..3521)
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                  /transl_table=11
                  /function="ampicillin resistance"
                  /evidence=experimental
                  /product="beta-lactamase"
                  /db_xref="PID:g531831"
                  /translation="MSIQHFRVALIPPEFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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QY 889 GCGGCGCTCTAAAGGATCCAGCTTACGTAGCGTGCATCGCGATGCGAGCTCATAGCTCTTCT 948

Db 1555 ATAGTGTACCTAAATTCATCAATCACTG 1581
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QY 949 ATAGTGTACCTAAATTCATCAATCACTG 975
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RESULT 5 SCU15970 5772 bp DNA PLN 18-SEP-1996
LOCUS Saccharomyces cerevisiae CSP2 gene, complete cds.
DEFINITION U15970
ACCESSION 9836895
NID
KEYWORDS
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryotes; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
Saccharomycetes.
REFERENCE 1 (bases 1 to 5772)
AUTHORS Supekova, L., Nelson, H. and Nelson, N.
TITLE A yeast manganese transporter related to the macrophage protein
involved in conferring resistance to mycobacteria
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 5105-5110 (1996)
MEDLINE 96209864
REFERENCE 2 (bases 1 to 5772)
AUTHORS Nelson, N.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1994) Nathan Nelson, Roche Institute of Molecular
Biology, 340 Kingsland St., Nutley, NJ 07110, USA
FEATURES
source
1..5772
Location/Qualifiers
/organism="Saccharomyces cerevisiae"
/strain="W303"
/db_xref="taxon:4932"
2462..3937
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2462..3937
/gene="CSP2"
/function="unknown"
/note="CDC1; similar to S. cerevisiae CDC1 gene product,
encoded by GenBank Accession Number X81813"
/codon_start=1
/db_xref="SGD:L0000241"
/db_xref="PID:9836896"
/translation="MYRNRSKSVLSTHSKSDDAHYKRSKSKSKSKRLRIYV
RYSIVLWGLISYVSVVYKRMKQWEDWPEGAESHVGLFADPQIMDEY
SYGPRQIVNYFTRIVDHYHRRNNKYQYIYLDPSNFFLGDLFDGGRNWDKQIMKE
YTRFQIFPKPLRTVMSLPGNHDIGFDTVVESSLORFSYFGETSSSLDAGNHTF
VLLDPLISLSDKTNVSRVPRQFLDNFAMGSHPLRLLTHVPLRDEPQTCGQGLRE
SKEPTPIQKHQYQVIENDISOELTKIQPEILFSGDDHDCQISHSPFQGTAKNA
QETIVKSCAMNGISRPAIQULSLNPSDLTMVNAAGYASKYQTELCYMPDPYKAI
RMYLGLLFSAFIAFYAHFFPKSFNNRVATIMRVFTPRDGNSTDLPLPTSISKSKS
KSLTHSKYAVNDRSIRKQFLVNAIVLFSVMPDIFYFYTVV"
BASE COUNT 1829 a 1015 c 1053 g 1875 t
ORIGIN

Query Match 8.2%; Score 82; DB 24; Length 5772;
Best Local Similarity 90.7%; Pred. No. 6.09e-38;
Matches 97; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Db 5642 TACAAGATCAAGCTTACGTACGCGTGCATCGCGATGCGAGCTCTCTATAGTGTACCC 5701
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QY 900 TAAAGATCAAGCTTACGTACGCGTGCATCGCGATGCGAGCTCTCTATAGTGTACCC 959
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Db 5702 TAAATTCATTCAGTGGCGCTGTTTACA-CGTCGTGACTGGGAAA 5747
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QY 960 TAAATTCATTCAGTGGCGCTGTTTACAACGCTCTGACTGGGAAA 1006
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RESULT 6 HIVU84854 2699 bp DNA VRL 23-FEB-1998
LOCUS HIV-1 strain M02 from USA, envelope glycoprotein (env) gene,
DEFINITION

partial cds.
U84854
92290120

Human immunodeficiency virus type 1.
Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 2699)
Connor, R.I., Korber, B.T.M., Graham, B.S., Hahn, B.H., Ho, D.D.,
Walker, B.D., Neumann, A.U., Vermund, S.H., Mestecky, J., Jackson, S.,
Penamora, E., Cao, Y., Gao, F., Kalams, S., Kunstman, K.J., McDonald, D.,
McWilliams, N., Trkola, A., Moore, J.P. and Wolinsky, S.M.
Immunological and virological analyses of persons infected by human
immunodeficiency virus type 1 while participating in trials of
recombinant gp120 subunit vaccines
J. Virol. 72 (2), 1552-1576 (1998)
98105804

2 (bases 1 to 2699)
Wolinsky, S. and Hahn, B.
Direct Submission
JOURNAL Submitted (13-JAN-1997) HIV Database, Los Alamos Nat'l Labs, Mail
Stop K710, Los Alamos, NM 87545, USA
Location/Qualifiers
1..2699
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/proviral
/strain="M02"
/db_xref="taxon:11676"
/note="subtype B; PBMC from an early vaccine-break control
patient"
130..2661
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130..2661
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/codon_start=1
/product="envelope glycoprotein"
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WEKATLFCASDAQYTERHNVWATHACVPTDPNPQEVLLNFTENFNWNNMYE
QMHEDIISLDQSLKPCVLTPLCVTLNCTDVTLSNTGVNTNKLNLTMKNCFSN
ITNIRDKKKEYALYTLIDVPIDNSDSYRLISGTSVITQACPKVTEPIPIHYC
APAGFAILKNNKTFESGKGVSTVQCTHGIRPVVSTOLLNGSLAEKVIIRSD
FSDNYKTIIVQLNESVAIDCIRPSNTRKSHIGCPRAFATGTIGDIRQAHCITNR
TWNQTLDRVIRKKKQFVNEKFEFGSGGDPPEIVHVSNGGFEFFYCNLTQFNIT
NTQNTTGNHTLPCRIKIIINMDEVKAMYPPIRGICRKSNTIGLLTRDGGENTN
HFDNPTIEIFPGGDMRNSRLYKVIKIEPLGVAPTAKRRVVQREKRVGIGA
MFLGPGAASVTLTVOARLLSGVIOQSNLLRAIEAQOHLLOLVYMGIKQ
LOARLVSRYLKDOOLGIGWCSGSLICTTTPWNASNSKSLINATWDTNWMOWEK
EISNVTLYKSLIEESQONQENLELLELDKWLNNFDITNWLWYIKFIMVIGG
LVGLRIVLVLISVNRVQGYSPLSFQTLRPLTPRGPDRPEGIEEDGERDKDRSLV
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ISLLNATATVAEAGTDRATEALQTAGRAILHHPRIROGLERALL"
2663..>2699
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/product="nef protein"
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BASE COUNT 941 a 474 c 640 g 644 t
ORIGIN

Query Match 7.0%; Score 70; DB 34; Length 2699;
Best Local Similarity 98.6%; Pred. No. 3.04e-29;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AGGTGACACTATAGAAGAGCTATGACGTGCGATGCGCGGTACGCTTGGATCCTCT 60
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Cp 960 AGGTGACACTATAGAAGAGCTATGACGTGCGATGCGCGGTACGCTTGGATCCTTT 901
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Db 61 AGAGCGGCCGCC 72

Cp 900 AGAGCGCGCC 889
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RESULT 7 HUMD4H12M3 98 bp mRNA PRI 01-DEC-1994
LOCUS Human HepG2 3' region MboI cDNA, clone hmd4h12m3.
DEFINITION D17247
ACCESSION g598848
NID gene signature.
KEYWORDS Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
SOURCE ORGANISM
Homo sapiens
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.

REFERENCE 1 (bases 1 to 98)
AUTHORS Matoba,K., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
TITLE The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
JOURNAL Gene 146 (2), 199-207 (1994)
PUBLISHER 94357437
REFERENCE 2 (bases 1 to 98)
AUTHORS Matoba,K.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo Matoba, Osaka University, Institute for Molecular and Cellular Bio; 1-3, Yamada-oka, Suita, Osaka 565, Japan (E-mail:matoba@inherit.imcb.osaka-u.ac.jp, Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922) Submitted (21-Jul-1993) to DDBJ by: Ryo Matoba
COMMENT Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2 Kizugawadai Kizu-cho, Soraku-gun, Kyoto Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321.

FEATURES
source
1..98
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
/sex="Male"
BASE COUNT 23 a 29 c 24 g 21 t 1 others
ORIGIN

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Best Local Similarity 87.8%; Pred. No. 8.14e-28;
Matches 78; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db 9 GCGCGCGCTCTAGAGGATCCAAAGCTTACGAGCGGTCATGCGAGCTCATAGCTCTTCTA 68
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Qy 890 GCGCGCGCTCTAAGAGATCCAAAGCTTACGAGCGGTCATGCGAGCTCATAGCTCTTCTA 949
Db 69 TAGANGCACCTAATCAATCAATCAATCGCC 97
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Qy 950 TAGTGTACCTAAATCAATCAATCAATCGCC 978

RESULT 8
LOCUS AR023813 538 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5795740.
ACCESSION AR023813
NID g3977107
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 538)
AUTHORS Platika,M., Platika,O. and Holland,J.F.
TITLE Pituitary differentiation factor and methods of use thereof

JOURNAL Patent: US 5795740-A 1 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..538
/organism="unknown"

BASE COUNT 129 a 123 c 137 g 141 t 8 others
ORIGIN

Query Match 6.3%; Score 63; DB 22; Length 538;
Best Local Similarity 86.5%; Pred. No. 2.80e-24;
Matches 83; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Db 441 GCGCGCGCTCTAGAGGATCCAAAGCTTACGAGCGGTCATGCGAGCTCATNN-TCTTCTT 499
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Qy 890 GCGCGCGCTCTAAGAGATCCAAAGCTTACGAGCGGTCATGCGAGCTCATGCTCTTCTA 949

Db 500 TAGTGTCAACCTAATCAATCAAT-CANTGGCGCGCGTT 534
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Qy 950 TAGTGTCACTAAATCAATCAATCACTGGCGCGTT 985

RESULT 9
LOCUS GI13951 398 bp DNA STS 22-DEC-1995
DEFINITION human STS SHGC-2867 clone pg-564.
ACCESSION GI13951
NID g1129690
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: CTCTGCGGAGGCAATTTTCAATC
Primer B: CAGGGTACTTTATCTCTAGCTC
STS size: 132
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 2 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute for Medical Research, Camden, NJ 08103.
Location/Qualifiers

FEATURES

source 1..398
/organism="Homo sapiens"
STS 110..241
primer_bind 110..132
primer_bind 110..132
BASE COUNT 101 a 83 c 100 g 104 t 10 others
ORIGIN
Query Match 5.9%; Score 59; DB 31; Length 398;
Best Local Similarity 88.2%; Pred. No. 1.74e-21;
Matches 67; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db 320 GCGCGNCTCTAGAGATCCAAAGCTTACCTAGCGTGCATNGGANGTCATAG-TCTTCT 378
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QY 889 GCGCGCGCTCTAAGAGATCCAAAGCTTACCTAGCGTGCATNGGANGTCATAGCTTCT 948
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QY 949 ATAGTGTCACTAAAT 964
ORIGIN
Query Match 10
LOCUS G41212 433 bp DNA STS 19-AUG-1998
DEFINITION LSCV119 Caprine BAC Capra hircus STS genomic, sequence tagged site.
ACCESSION G41212
NID 93435060
KEYWORDS STS
SOURCE goat.
ORGANISM Capra hircus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;
Capra.
REFERENCE 1 (bases 1 to 433)
Vainan,D., Schibler,L., Oustry-Vainan,A., Pailhoux,E., Furet,J.-P.,
Goldammer,T., Cotinot,C., Schwerin,M., Fellous,M. and Cribiu,E.P.,
High-resolution human/goat comparative map of the goat
Pollux/Intersex Syndrome (PIS): The human homologue is contained in
a human YAC from HSA3q23
Unpublished (1999)
JOURNAL
COMMENT
Contact: Edmond P. Cribiu
Laboratoire de Genetique biochimique et de Cytogetenetique
Institut National de la Recherche Agronomique
Centre de Recherche INRA de Jouy-en-Josas, 78352 Jouy-en-Josas,
France
Tel: 33134652672
Fax: 33134652478
Email: cribie@biotec.jouy.inra.fr
Primer A: CAAGCTACAGTCTATAGGGTC
Primer B: CTACACTGGCCAGAGGATTC
STS size: 155
PCR Profile:
Presoak: 94 °C for 5 minutes
Denaturation: 94 °C for 15 seconds
Annealing: 58 °C for 20 seconds
Polymerization: 72 °C for 20 seconds
PCR cycles: 30
Thermal cycler: MJ Research or Perkin-Elmer Cetus
Protocol:
Template: 30-100 ng
Primer: each 1 uM
dGTP, dCTP, dTTP: 100mM, dATP: 10mM + alpha P33 dATP 0.5 uCi
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2 mM
(NH4)2SO4: 20mM
Tween20: 0.01% w/v
Tris-HCl: 75 mM
pH: 9

Chromosome localization : 1q43.
Location/Qualifiers
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/strain="Saanen"
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fragments (average size 150 kb)"
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/clone_lib="Caprine BAC"
/sex="male"
/tissue_type="skin"
/cell_type="fibroblast"
/cell_line="CAT2"
/dev_stage="adult"
71..225
STS primer_bind 71..91
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BASE COUNT 116 a 126 c 108 g 83 t
ORIGIN
Query Match 5.8%; Score 58; DB 31; Length 433;
Best Local Similarity 96.8%; Pred. No. 8.55e-21;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 292 TTCTATAGTGTCACTAAATCCAAATTCACCTGGCGTCTGTTTACAACTGCTGACTGGGA 351
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QY 945 TTCTATAGTGTCACTAAATTCAAATTCACCTGGCGTCTGTTTACAACTGCTGACTGGGA 1004
Db 352 AA 353
QY 1005 AA 1006
ORIGIN
RESULT 11
LOCUS PSVSPORT 3160 bp DNA circular SYN 24-MAY-1995
DEFINITION Cloning vector pSVSPORT1 beta-lactamase gene, complete cds.
ACCESSION U14626
NID 9540252
KEYWORDS Cloning vector pSVSPORT1.
SOURCE Cloning vector pSVSPORT1
ORGANISM Cloning vector pSVSPORT1
REFERENCE 1 (sites)
AUTHORS D'Alessio,J.M.
TITLE Life Technologies, Inc. Catalogue
JOURNAL Unpublished (1994)
REFERENCE 2 (bases 1 to 3160)
AUTHORS Horton,M.E.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1994) Mary E. Horton, Life Technologies, Inc.,
Technical Services, 8400 Helgeman Court, Gaithersburg, MD
20884-9980, USA
FEATURES
source 1..3160
Location/Qualifiers
/organism="Cloning vector pSVSPORT1"
/db_xref="taxon:40160"
23..166
enhancer 170..232
promoter 242..257
TATA_signal 260..286
rep_origin 586..723
intron 912..919
polyA_signal 941..948
polyA_signal 1146..1170
rep_origin complement(2003..2863)
CDS
/codon_start=1
/transl_table=1
/function="ampicillin resistance"
/evidence="experimental"
/product="beta-lactamase"
/db_xref="PID:g540253"
/translation="MSIQHFRVALIPEFAAFLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILSFEPPEERPFMMSTFKVLICGAVLSIDAGQEQLGRRIRHYSQNDLVE

BASE COUNT 820 a 775 c 724 g 841 t
ORIGIN
YSPVTEKHLTGDMTVRELCSSAATMSDNTAANLLTTTGGPKELAFLEHNMGDHVTRL
DRWEPENEAIPNDRDRTMPVAMATTLKLLTGELLTLASQQQLIDWAEADKVGPL
LRSLPACGWFADKSGAGSRGIIAALGPDGKPSRIWVITTGQATMDERNRQIA
EIGASLKHNM

Query Match 5.7%; Score 57; DB 32; Length 3160;
Best Local Similarity 98.3%; Pred. No. 4.19e-20;
Matches 58; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 416 TCGGGCGGCTCTAGAGGATCAAGCTTACGTCACGCGTCGACGTCATAGCTCT 474
|||||
Qy 887 TCGGGCGGCTCTAAAGATCAAGCTTACGTCACGCGTCGACGTCATAGCTCT 945
|||||

RESULT 12 CSPATATLP 1297 bp RNA PLN 30-SEP-1997
LOCUS Cucumis sativus mRNA for patatin-like protein, partial.
DEFINITION Y12793
VERSION 2
G2462264
WORDS esterase; patatin.
SOURCE cucumber.
ORGANISM Cucumis sativus

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Violales; Cucurbitaceae; Cucumis.
REFERENCE 1 (bases 1 to 1297)
PREISIG-MUELLER, R., MAY, C., HOEHNE, M., GNAU, P. and KINDL, H.
TITLE Is the patatin-like protein localized to lipid bodies involved in
the mobilization of fat reserves?
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1297)
KINDL, H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-1997) H. Kindl, FB Chemie Universitaet Marburg,
Hans-Meerwein-Strasse, 35043 Marburg, FRG

FEATURES
source
1..1297
/organism="Cucumis sativus"
/db_xref="taxon:3659"
/tissue_type="cotyledon"
/clone_lib="psport"
/clone-"cshsp70291"
<1..1218
/function="mobilization of fat during seed germination"
/codon_start=1
/product="patatin-like protein"
/db_xref="PID:e316871"
/db_xref="PID:g2462265"

translation="PRVRFSLVLLTMVADFAGKMTITLISIDGGIRGIIPSIIILA
FLESKLOEDGPDVRIADYFDVAGTSTGLVTSMLTAPDKNNRPLYSASDIALFYIE
HAKIFPQNVFLASLVNFGKMGPKYNGLYLRSLIRGLLGDITLKOTLSOVIPAF
DIKLOPVETIEAKSELKNPKLADVCISTSAAPTELPGVEFOTKDSKGNRVEM
VDGVAANNPILAAHTVTKEMSLRHSSELLKIKPMETERMLVLSLGTGPKNDEKY
SAAKASKMGLDWYTHGGGTPIVDIFSDASADWDYHISFISQSDCHKNRYLIQDDT
LSGEVSSVDIAENLNLIIYVGENLLKPLSRVNLSESGKFEPLDAGKTNEQALAEFA
KMLSNRKLRLSP"
BASE COUNT 419 a 228 c 270 g 380 t
ORIGIN

Query Match 5.6%; Score 56; DB 24; Length 1297;
Best Local Similarity 98.3%; Pred. No. 2.04e-19;
Matches 57; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1240 GCGGCGGCTCTAGAGGATCAAGCTTACGTCACGCGTCGACGTCATAGCTCTT 1297
|||||
Qy 889 GCGGCGGCTCTAAAGATCAAGCTTACGTCACGCGTCGACGTCATAGCTCTT 946
|||||

RESULT 13 G14155 414 bp DNA STS 22-DEC-1995
LOCUS human STS SHGC-6182 clone pg-2782.
DEFINITION

ACCESSION G14155
NID g1129894
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Homini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
MYERS, R.M.
JOURNAL Unpublished (1995)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: TCCACAAACAGTAAGGAG
Primer B: CAAGGTATGGTACGCTGACT
STS size: 121
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 58 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

plasmid clones, generated from a lymphoblastoid cell line from a
human male. Localized to human chromosome 15 by analysis on the
NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute
for Medical Research, Camden, NJ 08103.

FEATURES
source
1..414
/organism="Homo sapiens"
STS
76..196
primer_bind 76..95
primer_bind complement(177..196)
BASE COUNT 100 a 102 c 87 g 104 t 21 others
ORIGIN

Query Match 5.5%; Score 55; DB 31; Length 414;
Best Local Similarity 87.2%; Pred. No. 9.85e-19;
Matches 82; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

Db 304 GCGGCGGCTTNGAGGATCAAGCTTACGTCACGCGTCGACGTCAGGTCATAGCTCTNC 363
|||||
Qy 889 GCGGCGGCTCTAAAGATCAAGCTTACGTCACGCGTCGACGTCATAGCTCTTC 947
|||||

Db 364 TTATAGTGTCAACTACTNCAATNNCACTGGCC 397
|||||
Qy 948 T-ATAGTGTCA-CCTAAATTCATT-CACITGGCC 978
|||||

RESULT 14 CVPGEM42 2746 bp DNA SYN 12-FEB-1996
LOCUS

CP	1006	TTTTCCCAAGTCCAGGACGTTGTAAAAACGACGGCCAGTGAATTCGATTTAGTGACACTATA	948
<hr/>			
RESULT	15		
LOCUS	GI6894	390 bp	DNA
DEFINITION	human STS SHGC-3196 clone pg-1108.	STS	05-MAR-1996
ACCESSION	GI6894		
NID	g1214320		
KEYWORDS	STS sequence; primer; sequence tagged site.		
SOURCE	human Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 5 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute for Medical Research, Camden, NJ 08103.		
ORGANISM	Homo sapiens		
	Eukaryota; Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choeanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 390)		
AUTHORS	Myers,R.M.		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Richard M. Myers Stanford Human Genome Center (SHGC) Stanford University School of Medicine Department of Genetics, M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689 Email: myers@shgc.stanford.edu		
<hr/>			
	Primer A: TTGTTGATGATCTGGCATATGTTAG Primer B: GGCCAAAAAGCGAAGCTCCATC STS size: 130 PCR Profile: Initial incubation: 94 degrees C for 90 seconds Denaturation: 94 degrees C for 15 seconds Annealing: 64 degrees C for 23 seconds Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal Cycler: Perkin Elmer 9600		
Protocol:	Template: 25 ng Primer: each 1 uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10 ul		
Buffer:	MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3		
FEATURES	Chromosome 5. Location/Qualifiers 1..390 /organism="Homo sapiens" 86..215 86..110 primer_bind primer_bind complement(193..215) BASE COUNT 111 a 76 c 80 g 108 t 15 others ORIGIN		
<hr/>			
Query Match	5.4%;	Score 54;	DB 31;
Best Local Similarity	85.7%;	Pred. No. 4.74e-18;	Length 390;
Matches	96;	Mismatches 10;	Indels 6;
Gaps	6;		
<hr/>			
Db	244	GGCGGCGNTCTAGAGGATCCCAAGCTTACGCGGTNCATGGACGCTCATAGCTCTCC	303
Qy	889	GGCGGCGCGCTCTAAGG-ATCCAAGCTTACGTAGCGGTGCATGGACGCTCATAGCTCTTC	947

Search completed: Fri May 14 07:43:41 1999
Job time : 1626 secs.